

SEQUENCE PROTOCOL

<110> Degussa AG

5 <120> New nucleotide sequences which code for the luxS gene

<130> 000457 BT

<140>

10 <141>

<160> 4

<170> PatentIn Ver. 2.1

15 <210> 1

<211> 1902

<212> DNA

<213> Corynebacterium glutamicum

20 <220>

<221> CDS

<222> (342)..(1610)

<223> luxS gene

25 <400> 1

ggtaggagta aaaaacgcag gagggcgctcg aaaagcgcttc gtctgtgccg taaccctgtga 60

cgcgctggccc gttggtatcg gcgacccagt cggtgcccag gtaggggcat gcggtttgtg 120

30 cggctgcgttc gaccgcgggc atcgcgctga tgggaaggcc gtcagtaatt acttcgggg 180

ctgcctcgtt ggtggtctct ggggttgctt caggttccgc cggggtacaa gcggtgagca 240

35 tgatggaagc agcaggata gtaggtaatg tacgacgcat gcagtcaagc ctagatcgtg 300

tgtcggaaac cggacgcaat gagctcgatg ttgaaacct t gtg aag aag ggg aat 356

Met Lys Lys Gly Asn 5

1

40 caa cgc ggc gcg atg agc tat cgc aac agt atc cac att ttg aca gcc 404

Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile His Ile Leu Thr Ala 20

10 15

45 tcg ctg ctg gtc gtg ggg ttg gga gct tcc gcc cgc ctg acg ctg ccg 452

Ser Leu Leu Val Gly Leu Gly Ala Ser Ala Arg Leu Thr Leu Pro 35

25 30

50 atg ttt gcg ctg tcg tgc gtg ctg ttg ttt gtg tgg ggt ttt ctg tac 500

Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val Trp Gly Phe Leu Tyr 50

40 45 50

55 ttc tat gga tca acc aaa cgc gta gat ttg agc cac gcc atg cag ctg 548

Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser His Gly Met Gln Leu 65

55 60 65

ggc tgg ctg ttt gtg ctg acg ctg gtg tgg att ttt atg gtg ccg atc 596

Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile Phe Met Val Pro Ile 85

70 75 80

	gtg ccc gtg tcc att tat ctg ctg ttc ccg ctg ttt ttc ctc tat cta	644
	Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu Phe Phe Leu Tyr Leu	
	90 95 100	
5	cag gtg atg cct gac gtg aga ggc att att gcg att ttg ggt gcg aca	692
	Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala Ile Leu Gly Ala Thr	
	105 110 115	
10	gcg att gcg att gcc agc cag tat tcc gtg ggg ttg acc ttt ggt ggt	740
	Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly Leu Thr Phe Gly Gly	
	120 125 130	
15	gtg atg ggt ccg gtg gtc tct gcg atc gtg acc gtg gct att gat tac	788
	Val Met Gly Pro Val Val Ser Ala Ile Val Thr Val Ala Ile Asp Tyr	
	135 140 145	
20	gcg ttc cgc acg ttg tgg cgg gtg aat aat gaa aag cag gaa ttg att	836
	Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu Lys Gln Glu Leu Ile	
	150 155 160 165	
	gat cag ttg att gaa act cgc tcc cag ctg gcg gtg acg gaa cga aat	884
	Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala Val Thr Glu Arg Asn	
	170 175 180	
25	gcg ggt att gct gcg gaa cgt caa cgt att gcg cat gaa att cat gac	932
	Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala His Glu Ile His Asp	
	185 190 195	
30	acg gtc gcc cag gga ctc tcc tcc att caa atg ctg ctg cat gtc tct	980
	Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met Leu Leu His Val Ser	
	200 205 210	
35	gaa cag gag att ctc gtt gct gag atg gaa gag aag cca aag gag gcg	1028
	Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu Lys Pro Lys Glu Ala	
	215 220 225	
40	atc gtg aag aag atg cgc ctt gcc cga caa aca gcc tcc gac aat ctc	1076
	Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr Ala Ser Asp Asn Leu	
	230 235 240 245	
	agt gag gct cgc gcg atg att gcg gcg ttg caa ccg gca gcg ctg tct	1124
	Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln Pro Ala Ala Leu Ser	
	250 255 260	
45	aaa acc tcc ttg gaa gca gca ctt cac cgc gtc aca gaa ccg ttg ttg	1172
	Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val Thr Glu Pro Leu Leu	
	265 270 275	
50	ggg att aat ttt gtg att tct gtc gac ggt gat gtt cgc caa ctg ccc	1220
	Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp Val Arg Gln Leu Pro	
	280 285 290	
55	atg aaa act gaa gcc acc ctt ctg cga att gct caa ggt gcg atc gga	1268
	Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala Gln Gly Ala Ile Gly	
	295 300 305	

aat gtg gcg aaa cat tca gag gcg aaa aac tgc cac gtg aca cta acc 1316
 Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys His Val Thr Leu Thr 325
 310 315 320

5 tac gaa gac aca gaa gta cgc ctt gat gtg gtt gat gac ggt gtg ggt 1364
 Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val Asp Asp Gly Val Gly 340
 330 335

10 ttt gag cct tcg gaa gtg tcc agt acc ccc gct ggc ctt ggc cat atc 1412
 Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala Gly Leu Gly His Ile 355
 345 350

15 ggc tta acc gca ttg cag cag cgt gcg atg gaa ttg cac ggc gaa gtt 1460
 Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu Leu His Gly Glu Val 370
 360 365

ata gtg gaa tct gca tat ggg cag ggt act gcg gta tct gca gca ttg 1508
 Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala Val Ser Ala Ala Leu 385
 375 380

20 ccg gtg gag cca cca gag ggg ttt gtc ggg gcg ccg gtt ttg gca gat 1556
 Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala Pro Val Leu Ala Asp 405
 390 395 400

25 tcg gac tca agt gct aca ggc gag gtt gaa cta agt tct cca act gac 1604
 Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu Ser Ser Pro Thr Asp 420
 410 415

30 gat gag taaggctaga ctaaagtacg attcatctgc tcatcgatac tcttgaaggc 1660
 Asp Glu

35 gcattttcat tcgaaacgaa gtgcgccatt gggaaggacc tagttcaaac aatgattcgc 1720
 gtgctgcttg ctgatgacca cgaaatcgtg aggctcggac tccgagctgt gctggaaagc 1780
 gccgaggaca ttgaagtgtt gggcgaagtc tccaccgccg aaggtgcggt gcaggcagcc 1840
 caagaaggcg gaatcgacgt catcttgatg gacctccgat tcgcccccg cgtccaagga 1900

40 ac 1902

<210> 2
 <211> 423
 45 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2
 Met Lys Lys Gly Asn Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile
 1 5 10 15
 His Ile Leu Thr Ala Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala
 20 25 30

55 Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val
 35 40 45
 Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser
 50 55 60

His Gly Met Gln Leu Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile
 65 70 75 80
 5 Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu
 85 90 95
 Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala
 100 105 110
 10 Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly
 115 120 125
 Leu Thr Phe Gly Gly Val Met Gly Pro Val Val Ser Ala Ile Val Thr
 130 135 140
 15 Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu
 145 150 155 160
 20 Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala
 165 170 175
 Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala
 180 185 190
 25 His Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met
 195 200 205
 Leu Leu His Val Ser Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu
 210 215 220
 30 Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr
 225 230 235 240
 35 Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln
 245 250 255
 Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val
 260 265 270
 40 Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp
 275 280 285
 Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala
 290 295 300
 45 Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys
 305 310 315 320
 50 His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val
 325 330 335
 Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala
 340 345 350
 55 Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu
 355 360 365

Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala
 370 375 380

5 Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala
 385 390 395 400

Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu
 405 410 415

10 Ser Ser Pro Thr Asp Asp Glu
 420

15 <210> 3
 <211> 20
 <212> DNA
 <213> Corynebacterium glutamicum

20 <220>
 <223> Primer luxS-int1

<400> 3
 tcgtgaccgt ggctattgat 20

25

<210> 4
 <211> 20
 <212> DNA

30 <213> Corynebacterium glutamicum

<220>
 <223> Primer luxS-int2

35 <400> 4
 cttgagcaat tcgcagaagg 20

40